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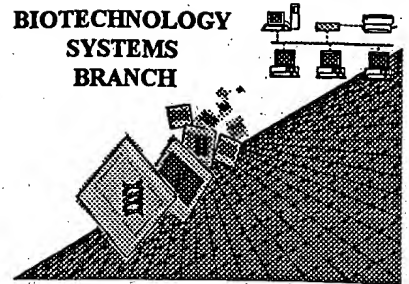
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/129,958_

Art Unit / Team No. : _1655_

Date Processed by STIC: _7/20/99_

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/129,958_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _✓_ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES) — Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — **Pleas d not use "Copy to Disk" function f PatentIn versi n 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.**

AKS-Biotechnology Systems Branch- 5/15/99

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> This Raw Listing contains the General Information
> Section and up to first 5 pages.   Does Not Comply
>   Corrected Diskette Needed

pp 1-2

```
 1    <110> APPLICANT: Mills, Allen P.
 2          Yurke, Bernard
 3          Platzman, Philip M.
 4    <120> TITLE OF INVENTION: ANALOG AND NEURAL NETWORK COMPUTATION USING DNA
 5    <130> FILE REFERENCE: LUTEC 0008
 6    <140> CURRENT APPLICATION NUMBER: US/09/129,958
 7    <141> CURRENT FILING DATE: 1998-08-06
 8    <150> EARLIER APPLICATION NUMBER: 09/078,761
 9    <151> EARLIER FILING DATE: 1998-05-15
10    <150> EARLIER APPLICATION NUMBER: 09/018,248
11    <151> EARLIER FILING DATE: 1998-02-03
12    <150> EARLIER APPLICATION NUMBER: 60/086,654
13    <151> EARLIER FILING DATE: 1998-05-26
14    <160> NUMBER OF SEQ ID NOS: 4
15    <170> SOFTWARE: PatentIn Ver. 2.0
16    <210> SEQ ID NO 1
17    <211> LENGTH: 10
18    <212> TYPE: DNA
19    <213> ORGANISM: Artificial Sequence
20    <220> FEATURE:
21    <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
22          analog oligonucleotide
23    <400> SEQUENCE: 1
24          agctatcgat                                                    10
25    <210> SEQ ID NO 2
26    <211> LENGTH: 34
27    <212> TYPE: DNA
28    <213> ORGANISM: Artificial Sequence
29    <220> FEATURE:
30    <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
31          analog oligonucleotide
32    <220> FEATURE:
33    <221> NAME/KEY: variation
34    <222> LOCATION: (34)
35    <400> SEQUENCE: 2
36          aatgcaagat cgaaatttat acgtttatct tacn)                        34
37    <210> SEQ ID NO 3
38    <211> LENGTH: 34
39    <212> TYPE: DNA
40    <213> ORGANISM: Artificial Sequence
41    <220> FEATURE:
42    <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
43          analog oligonucleotide
44    <220> FEATURE:
```

W-->

an explanation of "n" is mandatory in <223> response (see item 10 on Err Summary Sheet, and see 1.823 of Sequence Rules)

1655

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION **US/09/129,958**

DATE: 07/20/1999
TIME: 16:36:07

Input Set: **I129958.RAW**

```
45   <221> NAME/KEY: variation
46   <222> LOCATION: (34)
47   <400> SEQUENCE: 3
48         aatgcaagat cgaaatttat acgtttatct tacn                    34
49   <210> SEQ ID NO 4
50   <211> LENGTH: 30
51   <212> TYPE: DNA
52   <213> ORGANISM: Artificial Sequence
53   <220> FEATURE:
54   <223> OTHER INFORMATION: Description of Artificial Sequence:  DNA based
55         analog oligonucleotide
56   <400> SEQUENCE: 4
57         aatgcaagat cgaaatttat acgtttatct                         30
```

same error

W-->

Line	?	Error/Warning	Original Text
36	W	"N" or "Xaa" used: Feature required	aatgcaagat cgaaatttat acgtttatct tacn
48	W	"N" or "Xaa" used: Feature required	aatgcaagat cgaaatttat acgtttatct tacn